

GH74_Ace — DYAEINPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGGSEPGGVTTGGTVAASADGSR
AviIII_Aac — DYAGNKPSPNIVRSGASDDYP — TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT

GH74_Ace — FVWAPGDPGQPVVYAVGFGNSWAASQGV PANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac — VLLMSSTSGALVSKSQG — TLTAVSSLPSGAVIASDKSDNTVFYGGGAGAIYVSKNTAT

GH74_Ace — TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI TGVSSAVNV
AviIII_Aac — SFTKTVS LGSSTTVNAIR AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGV TAGWSF

GH74_Ace — GFGKSAPGSSYPVAVFVGTIGGVTGAYRSDDCGTTWVLINDDQHGYGN WQQAITGDHAN
AviIII_Aac — GFGKASSTGSYVVIYGFETIDGAAGLFKSEDAGTNWQVSDASHGFCGSGSANVVNGDLQT

GH74_Ace — LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac — YGRVFRGHERPGHLLRQSQRERAG

2. (Previously Amended) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.

3. (Previously Cancelled)

4. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.

5. (Previously Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.

6. (Previously Amended) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.

7. (Previously Amended) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Previously Amended) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.
9. (Previously Amended) The composition of claim 1 wherein said AvIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.
10. (Previously Amended) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.
11. (Previously Amended) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.
12. (Previously Amended) An isolated AvIII peptide having a polypeptide sequence of SEQ ID NO: 1.
13. (Cancelled)
14. (Previously Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the AvIII polypeptide of claim 1.
15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]
- 16-27 (Cancelled)
28. (Previously Amended) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:
 - a) a polypeptide sequence of SEQ ID NO: 3;
 - b) a polypeptide sequence of SEQ ID NO: 4;

- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Previously Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously Amended) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Original) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Original) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (New) The composition of claim 1 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII_Aac):

GH74_Ace ATTQPYTWSVNAIGGGG-FVDGIVFNEGAGILYVRTDGGIMMYRDAANGRWRAAPLLDWVG
Avilll_Aac AASQAYTWKNVVTTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
*** **

GH74_Ace WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPKLG
Avilll_Aac NDTWHDWGIDALATDPVDTDRVYVAVGMYNEDPNVGSILRSTDQGDWTETKLPFKVG
** * ..*

GH74_Ace GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFDPVGTIANPTD
Avilll_Aac GNMPGRGMGERLAVDPNKNLSILYFGARSHGLWKSTDYGATWSNVTSFTWTGTIFYQDSSS

GH74_Ace TTGYQSDIQGVVWVAFDKSSSLGQASKTFIVGVADPNPVFWSRDGGATWQAVPGAP-T
Avilll_Aac T--YTSDPVGIAVWTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
* ** *

GH74_Ace GFIPHKGVFPVNHVLIATSNTGGPYDGSSGDVWKFSVTSGTWTRISVPSTDTANDYF
Avilll_Aac GFLPHKGVLSPEEKTLIYSYANGAGPYDGTNGTVHKYNIISGVWTDISP---TSLASTYY
***** *

GH74_Ace GYSGLTIDRQHPNTIMVATQISWWPDTHFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS
Avilll_Aac GYGGLSVDLQVPGLTMVAALNCWWPDELIFRSTDGATWSPIEWENGYPSINYYSYDIS
** *** *

GH74_Ace AEPWLTFGVQPNNPPVSPKLGWMDAMPAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
Avilll_Aac NAPWIQDITSTQDFP--VRVGWMVEALAPDFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
** ..*

GH74_Ace HIAPMVKGLEETA VNDLISPPSGAPLISALGDLGGFTHADVTA VPSTIFTSPVFTTGTSV
Avilll_Aac TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI
..*** *

GH74_Ace DYAE LNPSII VRAGSFDPSSQPNDRHVAFSTDGGKNWFQGGSEPGGVTTGGTVAASADGSR
Avilll_Aac DYAGNKPSNIVRSGASDDYP-----TLALSSNFGSTWYADYA ASTSTGTGAVALSADGDT
*** **

GH74_Ace FVWAPGDPGPVVYAVGFGNWSAASQGV PANAQIRSDRVNP KTFYALSNGTFYRSTDGGV
Avilll_Aac VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSGAGAIYVSKNTAT
..* ** *

GH74_Ace TFQPVAAGLPSSGAVGMFMHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
Avilll_Aac SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
.* ** *

GH74_Ace GFGKSAPGSSYP AVFVVGTTGGVTGAYRSDDCGTTWVLINDDQH QYGN-WGQA ITGDHAN
Avilll_Aac GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT

GH74_Ace LRRVYIGTNGRGIVYGDIGGAPSG
Avilll_Aac YGRVFRGHERPGHLLRQSQRREPAG
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48. (New) The composition of claim 47 wherein said AvIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (New) A composition comprising a substantially purified AvIII peptide having at least 99% identity to SEQ ID NO. 1, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (New) The composition of claim 49 wherein said catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII_Aac):

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GH74_Ace  ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AvIII_Aac  AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
          ...*****...

GH74_Ace  WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AvIII_Aac  NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDWTETKLPFKVG
          ..*...*****...

GH74_Ace  GNMPGRGMGERLAVDPNNDNIFYGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AvIII_Aac  GNMPGRGMGERLAVDPNKNISILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYFQDSSS
          *****...

GH74_Ace  TTGYQSDIQGVVWVAFDKSSSSSLGQASKTIFVGVADPNPNPVFWSRDGGATWQAVPGAP-T
AvIII_Aac  T--YTSDPVGIAWVTFDSTSGSSSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
          *...*****...

GH74_Ace  GFIPHKGVFDPVNHVLIATSNTGGPYDGSSGDVWKFVSTSGTWTRISPVPSTDTANDYF
AvIII_Aac  GFLPHKGVLSPEEKTLIYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
          *****...

GH74_Ace  GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS
AvIII_Aac  GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDGATWSPIWEWNGYPSINYYYSYDIS
          *****...

GH74_Ace  AEPWLTFGVQPNPPVSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AvIII_Aac  NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNH
          **...*****...

GH74_Ace  HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AvIII_Aac  TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLAAPNQAYHTPTYGTTNGI
          :...*****...

GH74_Ace  DYAEINPSIIVRAGSFDPSQPNDRHVAFSTDGGKNWFQSGEPGGVTTGGTVAASADGSR
AvIII_Aac  DYAGNKPSNIVRSGASDDYP----TLALSSNFGSTWYADYAASSTGTGAVALSADGDT
          ***...*****

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GH74_Ace      FWWAPGDPGQPVVYAVGFGNSWAASQGVPANAIQRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac    VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSGAGIYVSKNTAT
               .:  . * * * . : * . . . . . . . . . . . . . . . . . . . .
GH74_Ace      TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac    SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
               . *  . . . . . . . . . . . . . . . . . . . . . . . . . .
GH74_Ace      GFGKSAPGSSYPAVFVVGTTGGVTGAYRSDDCGTTWVLINDDQHQQYGN-WGQAITGDHAN
AviIII_Aac    GFGKASSTGSYYVVIYGFFTTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVGNDLQT
               ***** . . . . . . . . . . . . . . . . . . . . . . . . . .
GH74_Ace      LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac    YGRVFRGHERPGHLLRQSQREPAG
               ** . . . . . . . . . . . . . . . . . . . . . . . . . .

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51. (New) The composition of claim 50 wherein said AvIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AvIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74 Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AvVIII peptide, said AvVIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain GH74 Ace has a sequence identical to SEQ ID NO. 3.